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OM protein - protein search, using sw model

Run on: November 3, 2005, 07:39:39 ; Search time 163 Seconds
(without alignments)
11.864 Million cell updates/sec

Title: US-10-726-366-1

Perfect score: 29

Sequence: 1 LPFFD 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	5	AAW32544	Anti-amy1
2	29	100.0	5	AA97167	Human Abe
3	29	100.0	5	AA62658	Alzheimer
4	29	100.0	5	AA26884	Decoy pep
5	29	100.0	5	AA29506	Amyloid b
6	29	100.0	5	AAU1179	Synthetic
7	29	100.0	5	ABU79017	Amyloidog
8	29	100.0	5	ABR42782	Amyloid b
9	29	100.0	5	AAO31194	Peptide #
10	29	100.0	5	ABW00151	Amyloid-b
11	29	100.0	5	ADI33443	Beta shee
12	29	100.0	5	ADJ71330	Pathologi
13	29	100.0	5	ADQ27002	Beta-shee
14	29	100.0	5	ADQ27003	Beta-shee
15	29	100.0	5	ADQ27004	Beta-shee
16	29	100.0	5	ADQ37394	Antifibri
17	29	100.0	6	AA29658	Amyloid b
18	29	100.0	6	AAE29742	Amyloid b
19	29	100.0	34	AA98338	WD40 pept
20	29	100.0	49	AA98338	WD40 pept
21	29	100.0	77	AA98338	WD40 pept
22	29	100.0	88	AA98338	WD40 pept
23	29	100.0	114	AA98338	WD40 pept
24	29	100.0	118	AA98338	WD40 pept
25	29	100.0	120	AA98338	WD40 pept

26	29	100.0	120	6	ABM54201	Propionib
27	29	100.0	164	2	AA936810	Amino aci
28	29	100.0	169	4	AA975548	Human col
29	29	100.0	201	7	ADM26249	Hyperther
30	29	100.0	202	4	AA979830	Corynebac
31	29	100.0	202	4	AA979829	Corynebac
32	29	100.0	202	4	AA979829	Corynebac
33	29	100.0	217	6	ADA36481	C glutami
34	29	100.0	220	5	AAU69702	Acinetoba
35	29	100.0	222	2	AA983339	Complete
36	29	100.0	225	5	ABW48230	Listeria
37	29	100.0	233	2	AAW22986	Human ser
38	29	100.0	240	3	AA823166	Human col
39	29	100.0	242	7	ABM73633	DNA clone
40	29	100.0	255	8	ADN48128	Thermococ
41	29	100.0	283	3	AA958345	Arabidops
42	29	100.0	287	3	AA958344	Arabidops
43	29	100.0	292	5	AA978578	Protease
44	29	100.0	295	5	AAU69700	Cell deat
45	29	100.0	305	5	AAU69699	Cell deat

ALIGNMENTS

RESULT 1
AAW32544
ID AAW32544 standard; peptide; 5 AA.

AC AAW32544;

DT 21-JAN-1998 (first entry)

DE Anti-amyloid peptide inhibiting abnormal protein folding.

KW Anti-amyloid peptide; iAbeta; abnormal protein folding inhibitor;
KW Alzheimer's disease; dementia; Down's syndrome; amyloidosis disorder;
KW human prion disease; Kuru; Creutzfeldt-Jakob disease;
KW Gerstmann-Strausler-Scheinker Syndrome; animal prion disease;
KW prion associated human neurodegenerative disease; scrapie;
KW spongiform encephalopathy; transmissible mink encephalopathy;
KW chronic wasting disease; mule; deer; elk; human.

OS Homo sapiens.

OS Synthetic.

PN WO9639834-A1.

XX 19-DEC-1996.

XX 06-JUN-1996; 96WO-US010220.

XX 07-JUN-1995; 95US-00478326.

XX 10-APR-1996; 96US-00630645.

XX (UJNY) UNIV NEW YORK STATE.

XX Sotoo-Jara C, Baumann MH, Frangione B;

XX WPI; 1997-051637/05.

XX New inhibitors of fibrillogenesis proteins or peptides - used for preventing, treating or detecting amyloidosis disorders such as Alzheimer's disease.

XX Claim 15; Page 38; 63pp; English.

XX A method has been developed for the prevention or treatment of a disorder or disease associated with the formation of amyloid or amyloid-like deposits, involving the abnormal folding of a protein or peptide. The method involves administering an inhibitory peptide which prevents the abnormal folding or which dissolves existing amyloid or amyloid-like deposits, where the peptide comprises a sequence of 3-15 amino acid

CC residues and has a hydrophobic cluster of at least 3 amino acids, where
 CC at least one of the 3 amino acids is a beta-sheet blocking amino acid
 CC residue selected from Pro, Gly, Asn and His. The present sequence
 CC represents a specifically claimed example of an anti- amyloid peptide
 CC which inhibits abnormal protein folding. The inhibitory peptide is
 CC capable of associating with a structural determinant on the protein or
 CC peptide to structurally block and inhibit the abnormal folding into
 CC amyloid or amyloid-like deposits. The method can be used for preventing,
 CC treating or detecting e.g. Alzheimer's dementia or disease, Down's
 CC syndrome, other amyloidosis disorders, human prion diseases such as Kuru,
 CC Creutzfeldt-Jakob disease, Gerstmann-Straussler- Scheinker Syndrome,
 CC prion associated human neurodegenerative diseases or animal prion
 CC diseases such as scrapie, spongiform encephalopathy, transmissible mink
 CC encephalopathy and chronic wasting disease of mule deer and elk
 XX
 XX Sequence 5 AA;

Query Match 100.0%; Score 29; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LPFFD 5
 Db 1 LPFFD 5

RESULT 2
 AAY97167
 ID AAY97167 standard; protein; 5 AA.

XX AC AAY97167;
 XX DT 19-DEC-2000 (first entry)
 XX DE Human Abeta binding domain.
 XX KW Alzheimer's disease; late onset Alzheimer's disease; LOAD; Abeta; LRP;
 XX KW low density lipoprotein receptor-related protein; A2M; neuropathy;
 XX KW alpha-2-macroglobulin; human.

XX OS Homo sapiens.
 XX PN WO200046246-A1.
 XX PD 10-AUG-2000.

XX PF 02-FEB-2000; 2000WO-US002412.

XX PR 02-FEB-1999; 99US-00241606.

XX PA (GEHO) GEN HOSPITAL CORP.

XX PI Tanzi RE, Kovacs DM, Saunders AJ;

XX DR WPI; 2000-514949/46.

XX DR N-PSDB; AAA52123.

XX PT Anti-LRP-A-beta peptide comprising an A-beta binding domain and a
 PT lipoprotein-receptor related protein binding domain, replaces alpha-2M
 PT function and suppresses expression of A2M-2, useful for the gene therapy
 PT of Alzheimer's disease.

XX PS Claim 5; Page 113; 120pp; English.

XX The most prevalent form of Alzheimer's disease is "late onset Alzheimer's
 CC disease" or LOAD. The alpha-2-macroglobulin gene (A2M) has been linked to
 CC LOAD and carriers of a particular mutation in A2M (a pentanucleotide
 CC deletion at the 5' splice site of the second exon encoding the bait
 CC region of A2M) are at increased risk of Alzheimer's disease. Strategies
 CC aimed at supplementing normal A2M function and activities in these
 CC individuals may serve as a means for therapeutically preventing, treating
 CC or even reversing Alzheimer's disease neuropathies. A new anti-LRP-Abeta
 CC peptide which can bind to Abeta and to LRP (low density lipoprotein

CC receptor-related protein) may be able to clear Abeta through LRP mediated
 CC endocytosis. The protein comprises an Abeta binding domain and a
 CC lipoprotein-receptor related protein (LRP) binding domain. The peptides,
 CC and nucleic acids encoding them are useful for the treatment of
 CC Alzheimer's disease and for identifying agents which may treat the
 CC disease

XX Sequence 5 AA;

Query Match 100.0%; Score 29; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LPFFD 5
 Db 1 LPFFD 5

RESULT 3

AAG62658
 ID AAG62658 standard; peptide; 5 AA.

XX AC AAG62658;

XX DT 17-SEP-2001 (first entry)

XX DE Alzheimer's amyloidosis beta-sheet breaker peptide inhibitor #2.

XX KW Beta-sheet breaker peptide; protein conformational disease; amyloid;
 XX KW Alzheimer's disease; FAF; Down' syndrome; amyloidosis disorder;
 XX KW prion disease; prion associated neurodegenerative disease; cyclic.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Misc-difference 1. .5
 XX FT /label= optionally D-form residue

XX FT Cross-links 1. .5
 XX FT /note= "optionally cyclise the molecule"

XX FT Modified-site 1

XX FT /label= OTHER
 XX FT /note= "optionally modified by acetyl or desamine, or
 CH2CH2 or CH2S via amide bond"

XX FT Modified-site 2

XX FT /label= OTHER
 XX FT /note= "optionally modified by CH2CH2 or CH2S via amide
 bond"

XX FT Modified-site 3

XX FT /label= OTHER
 XX FT /note= "optionally modified by methyl"

XX FT Modified-site 4

XX FT /label= OTHER
 XX FT /note= "optionally modified by methyl or by CH2S via
 amide bond"

XX FT Modified-site 5

XX FT /label= OTHER
 XX FT /note= "optionally C-terminal amine or alcohol"

XX PN WO200134631-A2.

XX PD 17-MAY-2001.

XX PF 04-NOV-2000; 2000WO-US030416.

XX PR 05-NOV-1999; 99US-0163911P.

XX PA (AXON-) AXONYX INC.

XX PI Soto-Jara C;

XX DR WPI; 2001-408068/43.

XX PT New peptide analogues and mimetics, useful by oral administration for the

PT treatment of Alzheimer's and prion disease by stabilization of the
 XX conformation of amyloidogenic peptide.
 PS Claim 2; Page 34; 49pp; English.
 CC The present invention relates to beta-sheet breaker peptide analogues
 CC capable of inhibiting beta-pleated sheet formation in amyloid beta-
 CC peptide. These are obtained by modification of a beta-sheet breaker
 CC peptide. They can be used to reduce the formation of amyloid or amyloid-
 CC like deposits involving abnormal folding into beta-sheet structures or
 CC conformational change in prion Pr protein. They are thus useful in the
 CC treatment of Alzheimer's disease, FAF, Down's syndrome, other amyloidosis
 CC disorders, prion diseases such as kuru, Creutzfeldt-Jakob disease,
 CC Gerstmann-Strausler-Scheinker syndrome, prion associated human
 CC neurodegenerative diseases, scrapie, spongiform encephalopathy,
 CC transmissible mink encephalopathy and chronic wasting disease of mule
 CC deer and elk. The present sequence is an optionally cyclic beta-sheet
 CC breaker peptide inhibitor of Alzheimer's amyloidosis described in the
 CC exemplification of the invention

XX Sequence 5 AA;

Query Match 100.0%; Score 29; DB 4; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LPFFD 5
 |||||
 Db 1 LPFFD 5

RESULT 4

AAE26884
 ID AAE26884 standard; peptide; 5 AA.

XX AC AAE26884;

XX DT 13-DEC-2002 (first entry)

XX DE Decoy peptide, DP24.

XX KW Decoy peptide; polyglutamine-containing protein; Huntington's disease;
 KW spinobulbar muscular atrophy; dentatorubral pallidolysian atrophy;
 KW spinocerebellar ataxia; Parkinson's disease; multiple system atrophy;
 KW Alzheimer's disease; Lewy body; Hallervorden-Spatz disease; neurotic;
 KW Creutzfeldt-Jakob disease; bovine spongiform encephalopathy; dementia;
 KW scrapie; neuroprotective; anticonvulsant.

XX OS Unidentified.

XX PN WO200264619-A2.

XX PD 22-AUG-2002.

XX PF 11-FEB-2002; 2002WO-US004060.

XX PR 09-FEB-2001; 2001US-0267898P.

XX PR 15-NOV-2001; 2001US-0334891P.

XX PA (MASI) MASSACHUSETTS INST TECHNOLOGY.

XX PI Ingram VM, Bankston J, Thumfort P, Blanchard BJ;

XX DR WPI; 2002-666988/71.

XX PT New decoy peptides inhibiting or reducing aggregation of polyglutamine-
 PT containing proteins, useful for treating Huntington's disease,
 PT Alzheimer's disease, Parkinson's disease, scrapie, and other
 PT neurodegenerative diseases.

XX PS Claim 1; Page 32; 71pp; English.

XX CC The invention relates to decoy peptides, inhibiting or reducing

CC aggregation of polyglutamine-containing proteins. The decoy peptides and
 CC the methods are useful for treating Huntington's disease, spinobulbar
 CC muscular atrophy, dentatorubral pallidolysian atrophy, spinocerebellar
 CC ataxia types 1, 2, 3 (Machado-Joseph disease), 6 and 7, Parkinson's
 CC disease, dementia with Lewy bodies, Lewy body variant of Alzheimer's
 CC disease, multiple system atrophy, Hallervorden-Spatz disease, Creutzfeldt
 CC -Jakob disease, variant Creutzfeldt-Jacob disease, bovine spongiform
 CC encephalopathy and scrapie. The present sequence is a decoy peptide

XX Sequence 5 AA;

Query Match 100.0%; Score 29; DB 5; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LPFFD 5

|||||

Db 1 LPFFD 5

RESULT 5

AAE29506

ID AAE29506 standard; peptide; 5 AA.

XX AC AAE29506;

XX DT 27-JAN-2003 (first entry)

XX DE Amyloid beta-protein related peptide #3.

XX KW Metallopeptide; neurotropic; amyloid beta-protein; Alzheimer's disease; AD;
 KW Prion's disease; oxytocin; angiotensin; vasopressin; neuroprotective;
 KW therapy; amyloid beta-protein related peptide.

XX OS Unidentified.

XX PN WO200264734-A2.

XX PD 22-AUG-2002.

XX PF 19-DEC-2001; 2001WO-US050075.

XX PR 19-DEC-2000; 2000US-0256842P.

XX PR 11-JUL-2001; 2001US-0304835P.

XX PR 04-OCT-2001; 2001US-0327835P.

XX PA (PALA-) PALATIN TECHNOLOGIES INC.

XX PI Sharma SD, Shi Y;

XX DR WPI; 2002-740699/80.

XX PT Determining secondary structure binding to desired targets within parent
 PT polypeptides that bind to targets, by constructing and complexing
 PT peptides to metal ions to form metallopeptides and screening the
 PT metallopeptides.

XX PS Claim 196; Page 99; 165pp; English.

XX CC The invention relates to a method for identification and determination of
 CC target-specific folding sites in peptides and proteins. The invention
 CC also relates to a method for determining a secondary structure binding to
 CC desired targets within parent polypeptides that bind to targets, by
 CC constructing and complexing peptides to metal ions to form
 CC metallopeptides and screening the metallopeptides. The method is useful
 CC for determining secondary structure binding to desired target within
 CC parent polypeptide with primary structure that binds to the target, where
 CC the target of interest is a receptor, antibody, toxin, enzyme, hormone,
 CC nucleic acid, intracellular protein domain of biological relevance or
 CC extracellular protein domain of biological relevance. A library of
 CC amyloid beta-protein related peptides is useful for the treatment of
 CC Alzheimer's disease (AD). A library of peptides targeting vasopressin,
 CC oxytocin or angiotensin receptor is useful for treating Prion's disease.

CC The present sequence is an amyloid beta-protein related peptide

XX Sequence 5 AA;

Query Match 100.0%; Score 29; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPFFD 5

Db 1 LPFFD 5

RESULT 6

AAU11779
ID AAU11779 standard; protein; 5 AA.

AC AAU11779;

DT 26-MAR-2002 (first entry)

DE Synthetic immunogenic non-amyloidogenic associated peptide.

XX Amyloid beta; non-amyloidogenic peptide; vaccine; immunogen;

KW Alzheimer's disease; amyloid fibril.

XX Synthetic.

XX WO200190182-A2.

XX 29-NOV-2001.

XX 22-MAY-2001; 2001WO-US016322.

XX 22-MAY-2000; 2000US-0205578P.

XX (UYNV) UNIV NEW YORK STATE.

XX Frangione B, Wisniewski T, Sigurdsson EM;

XX WPI; 2002-106186/14.

XX Novel isolated synthetic immunogenic but non-amyloidogenic peptide homologous to amyloid beta, useful for inducing immune response to amyloid beta peptides and amyloid deposits.

XX Disclosure; Page 69; 69pp; English.

XX The invention relates to an isolated synthetic immunogenic but non-amyloidogenic peptide homologous to amyloid beta. The peptide may be conjugated to polymer molecule. Antibodies raised against the peptides are also included. The peptide is useful for inducing an immune response to amyloid beta peptides and amyloid deposits and therefore treating Alzheimer's disease. The antibody is useful for reducing the formation of amyloid fibrils and deposits. The peptide has a reduced ability to adopt a beta-sheet conformation as an antigenic source, and a much lower risk of leading to any toxic effects in humans. The present sequence is a peptide included in the sequence listing but not mentioned any where else in the specification

XX Sequence 5 AA;

Query Match 100.0%; Score 29; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPFFD 5

Db 1 LPFFD 5

RESULT 7

ABU79017

ID ABU79017 standard; peptide; 5 AA.

XX AC ABU79017;

DT 17-JUN-2003 (first entry)

DE Amyloidogenic Amyloid A peptide #7.

XX Amyloid formation; amyloid-like deposit; Alzheimer's disease; pathological beta-sheet-rich conformation; Down's syndrome; amyloidosis disorder; human prion disease; kuru; CJD; Creutzfeldt-Jakob disease; Gerstmann-Strausler-Scheinker syndrome; GSS; prion associated human neurodegenerative disease; animal prion disease; scrapie; spongiform encephalopathy; transmissible mink encephalopathy; chronic wasting disease.

XX Homo sapiens.

XX US6462171-B1.

XX 08-OCT-2002.

XX 12-DEC-1996; 96US-00766596.

XX 07-JUN-1995; 95US-00478326.

XX 10-APR-1996; 96US-00630645.

XX (UYNV) UNIV NEW YORK STATE.

XX Soto-Jara C, Baumann MH, Frangione B;

XX WPI; 2003-379012/36.

XX Novel inhibitory peptides which inhibit and structurally block abnormal folding of protein into amyloid or amyloid-like deposit and into pathological beta-sheet rich conformation, useful for treating Alzheimer's disease.

XX Claim 1; Col 33-34; 51pp; English.

XX The invention describes an isolated inhibitory peptide (I) which interacts with a hydrophobic beta-sheet forming cluster of amino acid residues on a protein or peptide for amyloid or amyloid-like deposit formation, and inhibits or structurally blocks the abnormal folding of proteins and peptides into amyloid or amyloid-like deposits and into pathological beta-sheet-rich conformation. (I) is useful for disorders or diseases associated with abnormal protein folding into amyloid or amyloid-like deposits or into pathological beta-sheet-rich precursors of such disorders, such as Alzheimer's disease, Down's syndrome, other amyloidosis (CJD), Gerstmann-Strausler-Scheinker syndrome (GSS), prion associated human neurodegenerative diseases as well as animal prion diseases such as scrapie, spongiform encephalopathy, transmissible mink encephalopathy and chronic wasting disease of mule deer and elk. (I) is also useful for detecting and diagnosing the presence or absence of amyloid or amyloid-like deposits in vivo and its precursors. This is the amino acid sequence of peptide associated with the inhibition of amyloid or amyloid like deposits

XX Sequence 5 AA;

Query Match 100.0%; Score 29; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPFFD 5

Db 1 LPFFD 5

RESULT 8

ABR42782

ID ABR42782 standard; peptide; 5 AA.

XX ABR42782;
 AC 08-SEP-2003 (first entry)
 DT
 DE Amyloid beta homologous beta-amyloidogenic peptide.
 DE
 DE Amyloid beta; amyloidosis; Alzheimer's disease; neurotropic;
 KW neuroprotective; immunogen; vaccine.
 KW
 XX Synthetic.
 OS
 XX WO2003045128-A2.
 PN
 XX 05-JUN-2003.
 PD
 XX 21-NOV-2002; 2002WO-US037634.
 PF
 XX 21-NOV-2001; 2001US-0331801P.
 PR
 XX (UUNY) UNIV NEW YORK STATE.
 PA
 XX Frangione B, Wisniewski T, Sigurdsson EM;
 PI
 XX WPI; 2003-505145/47.
 DR
 XX New synthetic immunogenic but non-deposit forming peptides, useful for
 FT inducing an immune response to prions, amyloids, amylin or amylin
 FT fibrils, particularly for treating e.g. Alzheimer's, scrapie or
 PT Creutzfeldt-Jacob disease.
 PT
 XX Disclosure; Page 218; 265pp; English.
 PS
 XX The present sequence is that of a non-amyloidogenic peptide with sequence
 CC homology to amyloid beta (see ABR42769). The peptide blocks fibril
 CC formation and induces in vivo disassembly of fibrillar amyloid beta
 CC deposits. The invention provides amyloid beta homologous, immunogenic but
 CC non-deposit-forming polypeptides that can be used to induce an immune
 CC response to amyloid beta peptides for use in reducing amyloidosis. The
 CC use of non-fibrillar/non-toxic amyloid beta polypeptides is a safer
 CC vaccination approach for humans
 CC
 XX Sequence 5 AA;
 SQ
 Query Match 100.0%; Score 29; DB 6; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LPFFD 5
 Db
 1 LPFFD 5
 RESULT 9
 AAO31194
 ID AAO31194 standard; peptide; 5 AA.
 AC
 XX AAO31194;
 AC
 XX 06-OCT-2003 (first entry)
 DT
 XX Peptide #2 of the invention.
 DE
 XX Prion; PrP; transmissible spongiform encephalopathy; neuroprotective;
 KW Creutzfeldt-Jacob disease; CJD; fibrillar deposit; therapy.
 KW
 XX Unidentified.
 OS
 XX Key Location/Qualifiers
 FH Modified-site 1 /note= "Optionally acetylated"
 FT Modified-site 5 /note= "Optionally C-terminal amide"
 FT

XX WO2003050139-A2.
 PN
 XX 19-JUN-2003.
 PD
 XX 09-DEC-2002; 2002WO-EP013915.
 PF
 XX 10-DEC-2001; 2001EP-00000733.
 PR
 XX (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
 PA
 XX Adessi C, Halazy S, Saborio G, Soto-Jara C;
 PI
 XX WPI; 2003-598070/56.
 DR
 XX Use of new and known prion inhibitor peptide in the preparation of a
 PT medicament for treating or preventing transmissible spongiform
 PT encephalopathy e.g. Creutzfeldt-Jacob disease.
 PT
 XX Example 2; Fig 5; 41pp; English.
 PS
 XX The invention relates to a prion (PrP) inhibitor peptide or its analogue
 CC which is used in the preparation of a medicament for the treatment or
 CC prevention of transmissible spongiform encephalopathies e.g. Creutzfeldt-
 CC Jakob disease (CJD). The invention is useful as a medicament and is used
 CC to treat or prevent transmissible spongiform encephalopathy in a subject
 CC e.g. human. It is also useful for dissolving the fibrillar deposits
 CC already formed in a subject. The present sequence is a peptide of the
 CC invention
 CC
 XX Sequence 5 AA;
 SQ
 Query Match 100.0%; Score 29; DB 6; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LPFFD 5
 Db
 1 LPFFD 5
 RESULT 10
 ABR00151
 ID ABR00151 standard; peptide; 5 AA.
 AC
 XX ABR00151;
 AC
 XX 15-JAN-2004 (first entry)
 DT
 XX Amyloid-beta fibrillogenesis inhibitory peptide (iAbeta) #4.
 DE
 XX Amyloid-like fibril deposit; prion related encephalopathy; gene therapy;
 KW Alzheimer's disease; amyloid-beta fibrillogenesis inhibitor; iAbeta;
 KW inhibitor.
 KW
 XX Unidentified.
 OS
 XX US2003087407-A1.
 PN
 XX 08-MAY-2003.
 PD
 XX 06-SEP-2002; 2002US-00235483.
 PF
 XX 07-JUN-1995; 95US-00478326.
 PR
 XX 10-APR-1996; 96US-00630645.
 PR
 XX 12-DEC-1996; 96US-00766596.
 PR
 XX (UUNY) UNIV NEW YORK STATE.
 PA
 XX Soto-Jara C, Baumann MH, Frangione B;
 PI
 XX WPI; 2003-616149/58.
 DR
 XX

PT New inhibitory peptide, useful for preparing a composition for
 PT diagnosing, preventing or treating disorders associated with amyloid-like
 PT fibril deposits, e.g. Alzheimer's disease, or prion related
 PT encephalopathies.

XX Example 1; Page 18; 52pp; English.

XX The invention relates to inhibitory peptide comprising a portion of at
 CC least three amino acid residues and a sequence predicted not to adopt a
 CC beta-sheet structure that associates with a hydrophobic beta-sheet
 CC cluster on a protein or peptide involved in the abnormal folding into a
 CC beta-sheet structure, to structurally block the abnormal folding of the
 CC protein or peptide. The inhibitory peptide is useful for preparing a
 CC composition for preventing, treating or detecting disorders or diseases
 CC associated with amyloid-like fibril deposits e.g. Alzheimer's disease and
 CC prion related encephalopathies. The invention is also useful in gene
 CC therapy. The present sequence is amyloid-beta fibrillogenesis peptide
 CC (Abeta). This peptide is used in the invention

XX Sequence 5 AA;

Query Match 100.0%; Score 29; DB 7; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPFD 5
 |||||
 Db 1 LPPFD 5

RESULT 11

ADI33443
 ID ADI33443 standard; peptide; 5 AA.

AC ADI33443;

XX 06-MAY-2004 (first entry)

XX Beta sheet breaking peptide to treat amyloidogenic disorders.

XX beta sheet breaking peptide; cell death; cytotoxic; beta amyloid fibril;
 KW protein folding; Alzheimer's disease; dementia pugilistica; head trauma;
 KW hereditary cerebral haemorrhage with amyloidosis of the Dutch type;
 KW HCHWA-D; vascular dementia; amyloid angiopathy; neurotropic;
 KW neuroprotective; haemostatic; cerebroprotective.

XX Synthetic.

Key Location/Qualifiers

FH Modified-site 1

FT /note= "N-terminal acetyl"

FT Modified-site 3..4

FT /note= "Optionally N-methylated."

FT Modified-site 5

FT /note= "C-terminal amide; Optionally N-methylated."

XX WO2004005336-A2.

XX 15-JAN-2004.

XX 07-JUL-2003; 2003WO-EP050287.

XX 08-JUL-2002; 2002EP-00100787.

XX 19-DEC-2002; 2002EP-00102834.

XX (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.

XX Soto-Jara C, Adessi C, Halazy S, Rueckle T;

XX WPI; 2004-099370/10.

XX New beta sheet breaking peptides useful for the treatment or prevention
 PT of Alzheimer's disease, dementia and disease associated with abnormal

PT protein holding into amyloid and amyloid-like deposits.

XX Claim 14; Page 28; 19pp; English.

XX This invention relates to novel beta sheet breaking peptides with
 CC improved pharmacological profiles. Specifically, it refers to peptides
 CC that exhibit beta sheet breaking activity such that they can prevent cell
 CC death induced by the deposition of cytotoxic beta amyloid fibrils. The
 CC present invention describes these compositions as useful in the
 CC manufacture of a medicament for the treatment or prevention of diseases
 CC associated with abnormal protein folding into amyloid and amyloid-like
 CC deposits, in particular they can be used to treat Alzheimer's disease,
 CC dementia pugilistica (including head trauma), hereditary cerebral
 CC haemorrhage with amyloidosis of the Dutch type (HCHWA-D) and vascular
 CC dementia with amyloid angiopathy. Accordingly, they exhibit activities
 CC such as neurotropic, neuroprotective, haemostatic and cerebroprotective.
 CC This peptide sequence is the beta sheet breaking peptide of the
 CC invention.

XX Sequence 5 AA;

Query Match 100.0%; Score 29; DB 8; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPFD 5
 |||||
 Db 1 LPPFD 5

RESULT 12

ADJ71330

ID ADJ71330 standard; peptide; 5 AA.

AC ADJ71330;

XX 06-MAY-2004 (first entry)

XX Pathologic modified prions-proteins PrPSC peptide #3.

XX Prion; PrPSC; prions protein; transmissible spongiform encephalopathy.

XX Synthetic.

XX WO2004005920-A2.

XX 15-JAN-2004.

XX 04-JUL-2003; 2003WO-DE002249.

XX 04-JUL-2002; 2002DE-01030141.

XX (PRIO-) PRIONTYPE GMBH.

XX (SCHL/) SCHLEUSSNER C.

XX Engemann C, Hoeschler K, Lehmann J, Gabert J, Krummrei U;
 WPI; 2004-108912/11.

XX Detecting pathological prions in live animals, useful for diagnosis of
 PT transmissible spongiform encephalopathy, using immobilized agent that
 PT binds to beta-sheets.

XX Claim 5; Page 10; 24pp; German.

XX The present invention relates to a method for detecting pathologically
 CC altered prion proteins (PrPsc), which comprises incubating a test sample
 CC with a solid carrier to which an agent is able to bind, removing unbound
 CC proteins, and detecting proteins bound to the agent. The method is used
 CC to diagnose transmissible spongiform encephalopathies in live animals,
 CC even shortly after infection. The present sequence is a PrPSC peptide
 CC used to demonstrate the method of the invention.

```
SQ Sequence 5 AA;
Query Match      100.0%; Score 29; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPFFD 5
DB 1 LPFFD 5

RESULT 13
ADQ27002
ID ADQ27002 standard; peptide; 5 AA.
XX
AC ADQ27002;
XX
DT 09-SEP-2004 (first entry)
XX
DE Beta-sheet breaking peptide.
XX
KW Beta-sheet breaking peptide; neuroprotective; nootropic; tranquilizer;
KW vulnerable.
XX
OS Synthetic.
XX
FH Key
FT Modified-site 1 Location/Qualifiers
FT Modified-site 3 /note= "N-terminal acetylation"
FT Modified-site 5 /note= "aza-phe"
FT Modified-site 5 /note= "C-terminal amide"
XX
PN WO2004050689-A2.
XX
PD 17-JUN-2004.
XX
PF 01-DEC-2003; 2003WO-EP015033.
XX
PR 02-DEC-2002; 2002EP-00102673.
XX
PA (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
XX
PI Lopez Areiza JJ, Rueckle T, Soto-Jara C;
XX
DR WPI; 2004-468549/44.
XX
PT New beta-sheet breaking peptides useful for the manufacture of a
PT medicament for the treatment or prevention of a disease or condition e.g.
PT Alzheimer's disease.
XX
PS Claim 7; Page 48; 52pp; English.
XX
CC The invention relates to beta-sheet breaking peptides of specified
CC formula or their chiral derivatives. The peptides are used for the
CC manufacture of a medicament for the treatment or prevention of a disease
CC or condition e.g. Alzheimer's disease, dementia pugilistica (including
CC head trauma), hereditary cerebral haemorrhage with amyloidosis of the
CC Dutch type (HCHWA-D) and vascular dementia with amyloid angiopathy,
CC disease associated with abnormal protein folding into amyloid and amyloid
CC -like deposits. The beta-sheet breaking peptide provides improved
CC pharmacological profile. The present sequence represents a specific
CC example of a beta-sheet breaking peptide.
XX
SQ Sequence 5 AA;
Query Match      100.0%; Score 29; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPFFD 5
DB 1 LPFFD 5

RESULT 15
ADQ27004
ID ADQ27004 standard; peptide; 5 AA.
XX
AC ADQ27004;
```

```
Db 1 LPFFD 5

RESULT 14
ADQ27003
ID ADQ27003 standard; peptide; 5 AA.
XX
AC ADQ27003;
XX
DT 09-SEP-2004 (first entry)
XX
DE Beta-sheet breaking peptide.
XX
KW Beta-sheet breaking peptide; neuroprotective; nootropic; tranquilizer;
KW vulnerable.
XX
OS Synthetic.
XX
FH Key
FT Modified-site 1 Location/Qualifiers
FT Modified-site 2 /note= "N-terminal acetylation"
FT Modified-site 5 /note= "aza-pro"
FT Modified-site 5 /note= "C-terminal amide"
XX
PN WO2004050689-A2.
XX
PD 17-JUN-2004.
XX
PF 01-DEC-2003; 2003WO-EP015033.
XX
PR 02-DEC-2002; 2002EP-00102673.
XX
PA (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
XX
PI Lopez Areiza JJ, Rueckle T, Soto-Jara C;
XX
DR WPI; 2004-468549/44.
XX
PT New beta-sheet breaking peptides useful for the manufacture of a
PT medicament for the treatment or prevention of a disease or condition e.g.
PT Alzheimer's disease.
XX
PS Claim 7; Page 48; 52pp; English.
XX
CC The invention relates to beta-sheet breaking peptides of specified
CC formula or their chiral derivatives. The peptides are used for the
CC manufacture of a medicament for the treatment or prevention of a disease
CC or condition e.g. Alzheimer's disease, dementia pugilistica (including
CC head trauma), hereditary cerebral haemorrhage with amyloidosis of the
CC Dutch type (HCHWA-D) and vascular dementia with amyloid angiopathy,
CC disease associated with abnormal protein folding into amyloid and amyloid
CC -like deposits. The beta-sheet breaking peptide provides improved
CC pharmacological profile. The present sequence represents a specific
CC example of a beta-sheet breaking peptide.
XX
SQ Sequence 5 AA;
Query Match      100.0%; Score 29; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPFFD 5
DB 1 LPFFD 5

RESULT 15
ADQ27004
ID ADQ27004 standard; peptide; 5 AA.
XX
AC ADQ27004;
```

```

XX 09-SEP-2004 (first entry)
XX Beta-sheet breaking peptide.
XX Beta-sheet breaking peptide; neuroprotective; nootropic; tranquilizer;
XX vulnerable.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 1 /note= "N-terminal acetylation"
XX Modified-site 2 /note= "aza-Pro"
XX Modified-site 3 /note= "aza-phe"
XX Modified-site 5 /note= "C-terminal amide"
XX WO2004050689-A2.
XX
XX 17-JUN-2004.
XX
XX 01-DEC-2003; 2003WO-EP015033.
XX
XX 02-DEC-2002; 2002EP-00102673.
XX
XX (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
XX Lopez Areiza JJ, Rueckle T, Soto-Jara C;
XX WPI; 2004-468549/44.
XX
XX New beta-sheet breaking peptides useful for the manufacture of a
XX medicament for the treatment or prevention of a disease or condition e.g.
XX Alzheimer's disease.
XX
XX Claim 7; Page 48; 52pp; English.
XX
XX The invention relates to beta-sheet breaking peptides of specified
XX formula or their chiral derivatives. The peptides are used for the
XX manufacture of a medicament for the treatment or prevention of a disease
XX or condition e.g. Alzheimer's disease, dementia pugilistica (including
XX head trauma), hereditary cerebral haemorrhage with amyloidosis of the
XX Dutch type (HCHWA-D) and vascular dementia with amyloid angiopathy,
XX disease associated with abnormal protein folding into amyloid and amyloid
XX -like deposits. The beta-sheet breaking peptide provides improved
XX pharmacological profile. The present sequence represents a specific
XX example of a beta-sheet breaking peptide.
XX
XX Sequence 5 AA;
XX
XX Query Match 100.0%; Score 29; DB 8; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
XX Qy 1 LPFFD 5
XX |||||
XX 1 LPFFD 5
XX
XX Search completed: November 3, 2005, 08:00:56
XX Job time : 169 secs

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 3, 2005, 07:52:15 ; Search time 38 Seconds
(without alignments)
12.660 Million cell updates/sec

Title: US-10-726-366-1

Perfect score: 29

Sequence: 1 LPFFD 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	184	2	shikimate kinase T
2	29	100.0	184	2	probable shikimate
3	29	100.0	208	2	hypothetical prote
4	29	100.0	222	2	hypothetical prote
5	29	100.0	225	2	two-component resp
6	29	100.0	225	2	two-component resp
7	29	100.0	231	2	hypothetical prote
8	29	100.0	237	2	two-component resp
9	29	100.0	281	2	hypothetical prote
10	29	100.0	287	2	hypothetical prote
11	29	100.0	308	2	conserved hypothet
12	29	100.0	314	2	homoserine kinase
13	29	100.0	327	2	hypothetical prote
14	29	100.0	328	2	hypothetical prote
15	29	100.0	334	2	hypothetical prote
16	29	100.0	344	2	hypothetical prote
17	29	100.0	354	2	hypothetical prote
18	29	100.0	359	2	glycolate oxidase
19	29	100.0	375	2	imidazoleglycerolp
20	29	100.0	387	2	protein F23N19.17
21	29	100.0	389	2	hypothetical prote
22	29	100.0	390	1	probable exonuclea
23	29	100.0	405	2	aspartate transami
24	29	100.0	407	2	aspartate transami
25	29	100.0	407	2	aspartate transami
26	29	100.0	417	2	phosphoribosyl-AMP
27	29	100.0	418	2	protein C44E4.3 [i
28	29	100.0	418	2	aspartate transami
29	29	100.0	449	2	probable aspartate

30	29	100.0	456	2	T06136	aspartate transami
31	29	100.0	456	2	C82785	hypothetical prote
32	29	100.0	461	2	S65665	actin-binding prot
33	29	100.0	461	2	S65666	actin-binding prot
34	29	100.0	502	2	E83353	xylulose kinase PA
35	29	100.0	537	2	G85021	protoporphyrinogen
36	29	100.0	545	2	T02005	protoporphyrinogen
37	29	100.0	557	2	T07116	protoporphyrinogen
38	29	100.0	585	2	S46034	hypothetical prote
39	29	100.0	598	2	T01720	hypothetical prote
40	29	100.0	659	2	C85016	hypothetical prote
41	29	100.0	730	2	B85013	hypothetical prote
42	29	100.0	730	2	T10539	hypothetical prote
43	29	100.0	775	2	T37848	probable cleavage
44	29	100.0	790	2	G90477	hypothetical prote
45	29	100.0	801	2	AE3032	conserved hypothet

ALIGNMENTS

RESULT 1

E81679

shikimate kinase TC0646 [imported] - Chlamydia muridarum (strain Nigg)

C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn

C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C:Accession: E81679

R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey,

, C.; Dodson, R.; Gwin, M.; Nelson, M.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,

Nucleic Acids Res. 28, 1397-1406, 2000

A>Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A:Reference number: A81500; MUID:20150255; PMID:10684935

A:Accession: E81679

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-184 <TF>

A:Cross-references: UNIPROT:Q9PK27; GB:AE002333; GB:AE002160; NID:g7190681; PIDN:AAF3947

A:Experimental source: strain Nigg (MoPn)

C:Genetics:

A:Gene: TC0646

C:Superfamily: shikimate kinase; shikimate kinase homology

Query Match 100.0%; Score 29; DB 2; Length 184;

Best Local Similarity 100.0%; Pred. No. 51;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPFFD 5

Db 33 LPFFD 37

RESULT 2

H71522

probable shikimate kinase II - Chlamydia trachomatis (serotype D, strain UW3/Cx)

C:Species: Chlamydia trachomatis

C>Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004

C:Accession: H71522

R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,

Science 282, 754-759, 1998

A>Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra

A:Reference number: A71570; MUID:9900809; PMID:9784136

A:Accession: H71522

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-184 <ARN>

A:Cross-references: UNIPROT:O84372; GB:AE001310; GB:AE001273; NID:g3328789; PIDN:AAC6796

A:Experimental source: serotype D, strain UW-3/Cx

C:Genetics:

A:Gene: arol

C:Superfamily: shikimate kinase; shikimate kinase homology

F:6-121/Domain: shikimate kinase homology <SKI>

Query Match 100.0%; Score 29; DB 2; Length 184;

Best Local Similarity	100.0%	Pred. No. 51;
Matches	5;	Conservative
0;	Mismatches	0;
Indels	0;	Gaps
0;		

Qy 1 LPFD 5
|||
33 LPFD 32

RESULT 3

T04796
Hypothetical protein F10M23.70 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C/Accession: T04796
R:Bevan, M.; Lecharny, A.; Chafidor, F.; Krivitzky, M.; Kreis, M.; Hoheisel, J.; Mewes, H.
submitted to the Protein Sequence Database, February 1999
A/Reference number: Z15385
A/Accession: T04796
A/Molecule type: DNA
A/Residues: 1-208 <BEV>
A/Cross-references: UNIPROT:Q9SZ14; EMBL:AL035440
A/Experimental source: cultivar Columbia; EAC clone F10M23
C/genetics:
A/Map position: 4
A/Introns: 24/3
A/Note: F10M23.70

Query Match 100.0%: Score 29: DB 2: Length 208:

Query Match	100.0%;	Score 25, 25	Length 200,
Best Local Similarity	100.0%;	Pred. No. 57;	
Matches	5;	Conservative	0;
Mismatches	0;	Mismatches	0;
Indels	0;	Indels	0;
Gaps	0;	Gaps	0;

Qy 1 LPFD 5
109 LPFD 113
Db

RESULT 4

H82794
hypothetical protein XF0543 [imported] - Xylella fastidiosa (strain 9a5c)
C/Species: Xylella fastidiosa
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C/Accession: H82794
R/anonymous, The Xylella fastidiosa Consortium for Nucleotide Sequencing
Nature 406, 151-157, 2000
A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A/Reference number: A832515; MUID:20355717; PMID:10910347
A/Note: for a complete list of authors see reference number A59328 below
A/Accession: H82794
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-222 <SIM>
A/Cross-references: UNIPROT:Q9PFM4; GB:AE003901; GB:AE003849; NID:g9105384; PIDN:AAF8335
A/Experimental source: strain 9a5c
R/Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, D.E.A.; Carraro, D.M.; Carrier, H.; Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitaajina, J.P.; Krieger, J.E.; Kuranae, E.E.; Laig Chado, M.A.; Madeira, A.M.B.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; P.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmeri, D.A.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawaak A.; Authors: da Silva, A.C.R.; da Silva, P.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira M.; Tsuchiko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovskii-Almeida, S.; Vettore, A.L.; Z A/Reference number: A59328
A/Contents: annotation
C/Genetics:
A/Gene: XF0543

Query Match

Best Local Similarity	100.0%;	Pred. No. 61;
Matches	5;	Mismatches 0; Indels 0; Gaps 0;
Conservative	100.0%;	Indels 0; Gaps 0;
Indels	0;	Gaps 0;
Gaps	0;	

Qy 1 LPFD 5
94 LPFD 98

RESULT 5

AII1292

C;Species: *Listeria monocytogenes* [str]
C;Species: *Listeria monocytogenes*
C;Date: 27-Nov-2001 #sequence_revision
C;Accession: AII1292
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
J.; Jones, L.M.; Karst, U.
Science 294 , 849–852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maubert,
O. C.; Schluteter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund,
A.; Title: Comparative genomics of *Listeria species*.
A;Reference number: AB1077; PMID:21537279; PMID:11679669
A;Accession: AII1292
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-225 <GLA>
A;Cross-references: UNIPROT:Q8Y6E2; GB:NC_003210; PIDN:CAC9823.1; PID:g16411199; GSPDB:
A;Experimental source: strain EGD-e
C;Genetics:
C;Superfamily: ompR protein; response regulator homology

Query Match	100.0%	Score 29	DB 2	Length 225
-------------	--------	----------	------	------------

Best Local Similarity	100.0%;	Pred. No. 62;	
Matches	5; Conservative	0; Mismatches	
Indels	0;	Gaps	0;

QY	1 LPFFD 5
Dh	55 LPFFD 5

RESULT 6

AG1664
two-component response regulator homolog lin1856 [imported] - *Listeria innocua* (strain C
C:Species: *Listeria innocua*
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AG1664
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Raquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Feihl, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A.; Title: Comparative genomics of *Listeria* species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AG1664
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-225 <GLA>
A:Cross-references: UNIPROT:Q92AR3; GB:AL592022; PIDN:CAC97087.1; PID:g16414358; GSPDB:G:
A:Experimental source: strain Clp11262
C:Genetics:
A:Gene: lin1856
C:Superfamily: ompR protein; response regulator homolog

Query Match	100.0%	Score 29	DB 2	Length 225
-------------	--------	----------	------	------------

Best Local Similarity	100.0%;	Pred. No. 62;	
Matches	5;	Conservative	0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPFD 5
db 55 LPFD 59

RESULT 7

H84535
hypothetical protein At2g16030 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: H84535
R:Lin, X.; Kaul, S.; Rounslev, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Niernan, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Frazer, C.M.; Venter, L.
Nature 402, 761-769, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: H84535
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-231 <STO>
A:Cross-references: UNIPROT:Q9XII4; GB:AE002093; NID:G4678200; PIDN:AAD26946.1; GSPDB:GN
C:Genetics:
A:Gene: At2g16030
A:Map position: 2

Query Match 100.0%; Score 29; DB 2; Length 231;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPFFD 5
Db 144 LPFFD 148

RESULT 8
D70032
two-component response regulator [YvcQ] homolog yvcP - Bacillus subtilis
C:Species: Bacillus subtilis
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: D70032
R:Kunst, F.; Ogawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
tech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Ser
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: D70032
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-237 <KUN>
A:Cross-references: UNIPROT:O06978; GB:Z99121; GB:AL009126; NID:G2635827; PIDN:CAB15477.
A:Experimental source: strain 168
C:Genetics:
A:Gene: yvcP
A:Superfamily: ompR protein; response regulator homology
C:Keywords: phosphoprotein
F:4-112/Domain: response regulator homology <RRH>
F:52/Binding site: phosphate (Asp) (covalent) #status predicted

Query Match 100.0%; Score 29; DB 2; Length 237;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPFFD 5
Db 55 LPFFD 59

RESULT 9
AC2095
hypothetical protein all2314 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AC2095
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AC2095
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-281 <KUR>
A:Cross-references: UNIPROT:Q8YUM6; GB:BA000019; PIDN:BAW74013.1; PID:gl7131406; GSPDB:G
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all2314

Query Match 100.0%; Score 29; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPFFD 5
Db 46 LPFFD 50

RESULT 10
T05338
hypothetical protein F1C12.211 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T05338
R:Bevan, M.; Terry, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.; De
ewes, H.W.; Mayer, K.F.X.; Schueller, C.
submitted to the Protein Sequence Database, April 1998
A:Reference number: 215408
A:Accession: T05338
A:Molecule type: DNA
A:Residues: 1-287 <BEV>
A:Cross-references: UNIPROT:O65443; EMBL:AL022224
A:Experimental source: cultivar Columbia; BAC clone F1C12
C:Genetics:
A:Map position: 4
A:Introns: 37/2; 116/2; 243/3; 269/3
A:Note: F1C12.211

Query Match 100.0%; Score 29; DB 2; Length 287;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPFFD 5
Db 65 LPFFD 69

RESULT 11
F95903
conserved hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) magapla
C:Species: Sinorhizobium meliloti
C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: F95903
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1,683-Kb pSymB megaplasmid from the N2-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: F95903
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-308 <KUR>

A; Cross-references: UNIPROT:Q92W51; GB:AL591985; PIDN:CA48894.1.; PID:gl5140367; GSPDB:B.1
A; Experimental source: strain 1021, megaplasmid pSymB
R; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, C.;
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A; Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A; Reference number: A96039; MUID:21368234; PMID:11474104
A; Contents: annotation
C; Genetics:
A; Gene: SMB20513
A; Genome: plasmid

Query Match 100.0%; Score 29; DB 2; Length 308;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPFFD 5
Db 49 LPFFD 53

RESULT 12
I64047
homoserine kinase (EC 2.7.1.39) - Haemophilus influenzae (strain Rd KW20)
C; Species: Haemophilus influenzae
C; Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C; Accession: I64047
R; Fleisschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
; D.M.; Brandon, R.C.; Pine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A; Authors: Gnehm, C.B.; McDonald, L.A.; Small, K.V.; Praser, C.M.; Smith, H.O.; Venter,
A; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A; Reference number: A64000; MUID:95350630; PMID:7542800
A; Accession: I64047
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-314 <TIGR>
A; Cross-references: UNIPROT:P44504; GB:U32694; GB:I42023; NID:gl573035; PIDN:AAC21766.1;
C; Superfamily: homoserine kinase
C; Keywords: ATP; phosphotransferase; threonine biosynthesis

Query Match 100.0%; Score 29; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPFFD 5
Db 170 LPFFD 174

RESULT 13
T20648
hypothetical protein F09C6.2 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C; Accession: T20648
R; Wortimore, B.
submitted to the EMBL Data Library, November 1996
A; Reference number: Z19305
A; Accession: T20648
A; Status: preliminary; translated from GB/EMBL/DBJ
A; Molecule type: DNA
A; Residues: 1-327 <MIL>
A; Cross-references: UNIPROT:O45329; EMBL:Z81496; PIDN:CA804070.1; GSPDB:GN00023; CESP:PC
A; Experimental source: clone F09C6
C; Genetics:
A; Gene: CESP:F09C6.2
A; Map position: 5
A; Introns: 38/2; 238/3

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 3, 2005, 07:40:19 ; Search time 169 Seconds
(without alignments)
15.150 Million cell updates/sec

Title: US-10-726-366-1

Perfect score: 29

Sequence: 1 LPFFD 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_eprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	41	Q8K408	Q8K408 rattus norv
2	29	100.0	71	Q64ZK7	Q64ZK7 bacteroides
3	29	100.0	132	Q8U320	Q8U320 pyrococcus
4	29	100.0	140	Q7PDS0	Q7PDS0 plasmodium
5	29	100.0	166	Q6AES3	Q6AES3 leifsonia x
6	29	100.0	168	Q7P0W1	Q7P0W1 chromobacte
7	29	100.0	168	Q7VXK4	Q7VXK4 bordetella
8	29	100.0	168	Q7W8Z3	Q7W8Z3 bordetella
9	29	100.0	168	Q7WKD6	Q7WKD6 bordetella
10	29	100.0	182	Q6N1M9	Q6N1M9 rhodospseudo
11	29	100.0	184	AROK_CHLMU	Q9PK27 chlamydia m
12	29	100.0	184	AROK_CHLTR	Q84372 chlamydia t
13	29	100.0	190	Q8XV61	Q8XV61 raietonia s
14	29	100.0	192	Q9FD35	Q9FD35 pseudomonas
15	29	100.0	200	Q890A9	Q890A9 lactobacill
16	29	100.0	201	HIS7_METKA	P58879 methanopyru
17	29	100.0	201	Q8L7N7	Q8L7N7 arabidopsis
18	29	100.0	201	Q98127	Q98127 rhizobium l
19	29	100.0	202	HIS7_COREF	Q8fn22 corynebacte
20	29	100.0	202	HIS7_CORGL	Q9fkj3 corynebacte
21	29	100.0	208	Q976L4	Q976L4 sulfobobus
22	29	100.0	208	Q9SZL4	Q9SZL4 arabidopsis
23	29	100.0	222	Q87B66	Q87B66 xyliella fas
24	29	100.0	222	Q9PFW4	Q9PFW4 xyliella fas
25	29	100.0	225	Q8Y6E2	Q8Y6E2 listeria mo
26	29	100.0	225	Q92AR3	Q92AR3 listeria mo
27	29	100.0	225	Q7IYS3	Q7IYS3 listeria mo
28	29	100.0	230	Q9CKJ1	Q9CKJ1 pasteurella
29	29	100.0	231	Q9XII4	Q9XII4 arabidopsis
30	29	100.0	231	Q988Q1	Q988Q1 clostridium
31	29	100.0	237	Q6FPX3	Q6FPX3 candida gla

32 29 100.0 237 2 Q75DJ3 Q75dj3 ashbya goss
33 29 100.0 237 2 Q06978 Q06978 bacillus su
34 29 100.0 247 2 Q07UT89 Q07UT89 rhodopirell
35 29 100.0 252 2 Q65WN9 Q65wn9 manheimia
36 29 100.0 255 2 Q98NS4 Q98ne4 rhizobium l
37 29 100.0 256 2 Q9N904 Q9n904 trypanosoma
38 29 100.0 262 2 Q8U419 Q8u419 pyrococcus
39 29 100.0 262 2 Q72EN9 Q72en9 desulfotovibr
40 29 100.0 274 2 Q9N4Y4 Q9n4y4 caenorhabdi
41 29 100.0 281 2 Q8YUM6 Q8yum6 anabaena sp
42 29 100.0 287 2 Q65443 Q65443 arabidopsis
43 29 100.0 296 2 Q85T23 Q85tz3 lithasia ja
44 29 100.0 302 2 Q86Z80 Q86z80 magnaporthe
45 29 100.0 306 1 DIMH_DROME Q9vaq5 drosophila

ALIGNMENTS

RESULT 1

Q8K408 PRELIMINARY; PRT; 41 AA.
AC Q8K408;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Truncated macrophage colony stimulating factor.
GN Name=Csf1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LEW tl;
RX MEDLINE=22069908; PubMed=12074592; DOI=10.1016/S0006-291X(02)00598-3;
RA Dobbins D.E., Sood R., Hashimoto A., Hansen C.T., Wilder R.L.,
RA Remmers E.F.;
RT "Mutation of macrophage colony stimulating factor (Csf1) causes
RT osteopetrosis in the tl rat.";
RL Biochem. Biophys. Res. Commun. 294:1114-1120(2002).
DR EMBL; AF514357; AAM54137.1;
SQ SEQUENCE 41 AA; 4178 MW; ID342C19BD18AA41 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPFFD 5
Db 13 LPFFD 17

RESULT 2

Q64ZK7 PRELIMINARY; PRT; 71 AA.
ID Q64ZK7;
AC Q64ZK7;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Bacteroides fragilis.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=817;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YCH46;
RA Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA Kuhara S., Hattori M., Hayashi T., Ohnishi Y.;
RT "Genomic analysis of Bacteroides fragilis reveals extensive DNA
RT inversions regulating cell surface adaptation.";

RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2004).
 DR EMBL; AP006841; BAD47069.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 71 AA; 7941 MW; 582FC7A3FABF40DB CRC64;

Query Match 100.0%; Score 29; DB 2; Length 71;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LPFFD 5
 Db 49 LPFFD 53

RESULT 3

Q8U320 PRELIMINARY; PRT; 132 AA.
 ID Q8U320
 AC Q8U320
 DT 01-JUN-2002 (TReMBLrel. 21, Created)
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Hypothetical protein PF0656.
 GN OrderedLocustNames=PF0656;
 OS *Pyrococcus furiosus*.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC *Pyrococcus*.
 OX NCBI_TaxID=2261;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Vci / DSM 3638 / ATCC 43587 / JCM 8422;
 RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
 RT "The complete sequence of the *Pyrococcus furiosus* genome."
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE010186; AAL80780.1; -.
 KW Complete proteome.
 SQ SEQUENCE 132 AA; 15765 MW; 2CABE074EB5393C5 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPFFD 5
 Db 123 LPFFD 127

RESULT 4

Q7PDS0 PRELIMINARY; PRT; 140 AA.
 ID Q7PDS0
 AC Q7PDS0
 DT 01-MAR-2004 (TReMBLrel. 26, Created)
 DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE tRNA-pseudouridine synthase B-related.
 GN Name=PY02575;
 OS *Plasmodium yoelii yoelii*.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=73239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=17XNL;
 RX PubMed=12368865; DOI=10.1038/nature01099;
 RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteau M.,
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
 RA Shalom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
 RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
 RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.;

RT "Genome sequence and comparative analysis of the model rodent malaria

RT parasite *Plasmodium yoelii yoelii*.
 RL Nature 419:512-519(2002). The sequence shown here is derived from an
 CC -!- CAUTION: EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AABL01000706; EAA22039.1; -.
 DR HSSP; Q9WZM0; 1R3E.
 DR GO; GO:0004730; P:pseudouridylylate synthase activity; IEA.
 DR GO; GO:0006336; P:RNA processing; IEA.
 DR InterPro; IPR002501; TruB__synth_N.
 DR Pfam; PF01509; TruB_N; 1.
 SQ SEQUENCE 140 AA; 16724 MW; 276DAC75A0590624 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 140;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPFFD 5
 Db 74 LPFFD 78

RESULT 5

Q6AES3 PRELIMINARY; PRT; 166 AA.
 ID Q6AES3
 AC Q6AES3
 DT 25-OCT-2004 (TReMBLrel. 28, Created)
 DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=Lxx12820;
 OS *Leifsonia xylii* (subsp. *xylii*).
 OC Bacteria; Actinobacteriia; Actinobacteridae; Actinomycetales;
 OC Micrococcales; Microbacteriaceae; *Leifsonia*.
 OX NCBI_TaxID=59736;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CTCB07;
 RX PubMed=15305603;
 RA Monteiro-Vitorello C.B., Camargo L.E.A., Van Sluys M.A.,
 RA Kitajima J.P., Truffi D., do Amaral A.M., Harakava R.,
 RA de Oliveira J.C.F., Wood D., de Oliveira M.C., Miyaki C.Y.,
 RA Takita M.A., da Silva A.C.R., Furlan L.R., Carraro D.M., Camarotte G.,
 RA Almeida N.F. Jr., Carrier H., Coutinho L.L., El-Dorry H.A.,
 RA Ferro M.I.T., Gagliardi P.R., Gigliotti E., Goldman M.H.S.,
 RA Goldman G.H., Kimura E.T., Ferro E.S., Kuramae E.E., Lemos E.G.M.,
 RA Lemos M.V.F., Mauro S.M.Z., Machado M.A., Marino C.L., Menck C.F.,
 RA Nunes L.R., Oliveira R.C., Pereira G.G., Siqueira W., de Souza A.A.,
 RA Tsai S.M., Zanca A.S., Simpson A.J.G., Brumbley S.M., Setubal J.C.;
 RT "The genome sequence of the Gram-positive sugarcane pathogen *Leifsonia*
 RT *xylii* subsp. *xylii*."
 RL Mol. Plant Microbe Interact. 17:827-836(2004).
 DR EMBL; AE016822; AAT89122.1; -.
 KW Complete proteome.
 SQ SEQUENCE 166 AA; 16670 MW; 2536DBD66856B56 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 166;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPFFD 5
 Db 68 LPFFD 72

RESULT 6

Q7P0W1 PRELIMINARY; PRT; 168 AA.
 ID Q7P0W1
 AC Q7P0W1
 DT 01-MAR-2004 (TReMBLrel. 26, Created)
 DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Hypothetical protein.

GN OrderedLocusNames=CV0454;
 OS Chromobacterium violaceum.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neiseeriales;
 OC Neiseeriaceae; Chromobacterium.
 OX NCBI_TaxID=536;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 12472 / DSM 30191;
 RX MEDLINE=22882880; PubMed=14500782; DOI=10.1073/pnas.1832124100;
 RA Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
 RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
 RA Alves-Gomes J.A., Andrade E.M., Avarepe J., de Araujo M.F.F.,
 RA Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
 RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
 RA Bordignon J., Brigido M.M., Brito C.A., Brocchi M., Burity H.A.,
 RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
 RA Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,
 RA Creczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
 RA Fantinatti F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,
 RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,
 RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangiro T.B.,
 RA Grattapaglia D., Griseard E.C., Hanna E.S., Jardim S.N., Laurino J.,
 RA Leoi L.C.T., Lima L.F.A., Loureiro M.P., Lyza M.C.C.P.,
 RA Madeira H.M.F., Manfio G.P., Maranhao A.O., Martins W.S.,
 RA di Mauro S.M.Z., de Medeiros S.R.B., Meisner R.V., Moreira M.A.M.,
 RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
 RA Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
 RA Pereira M., Pinto L.S.R., Pinto L.S., Porto J.I.R., Potrich D.P.,
 RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
 RA Santos E.B.P., Santos F.R., Schneider M.P.C., Seanez H.N.,
 RA Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
 RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
 RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,
 RA Vettore A., Wassem R., Zaha A., Simpson A.J.G.;
 RT "The complete genome sequence of Chromobacterium violaceum reveals
 RT remarkable and exploitable bacterial adaptability";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665 (2003).
 DR EMBL; AE016911; AAQ59132.1; -;
 DR InterPro; IPR000504; RNA rec_mot.
 DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 168 AA; 18411 MW; 16243267D86783D4 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 168;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LPFFD 5
 Db 127 LPFFD 131

RESULT 7
 Q7VXK4 PRELIMINARY; PRT; 168 AA.
 ID Q7VXK4
 AC Q7VXK4
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DE Lipoprotein signal peptidase (EC 3.4.23.36).
 GN Name=lpA; OrderedLocusNames=BPI752;
 OS Bordetella pertussis.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Alcaligenaceae; Bordetella.
 OX NCBI_TaxID=520;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Tohama 1 / ATCC BAA-589 / NCTC 13251;
 RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
 RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
 RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
 RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
 RA Achman M., Atkin R., Baker L., Basham D., Bason N., Cherevach I.,
 RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
 RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
 RA Leather S., Moulé S., Norberczak H., O'Neil S., Ormond D., Price C.,
 RA Rabinowitch E., Rutter S., Sanders M., Saunders D., Seeger K.,
 RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
 RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
 RT "Comparative analysis of the genome sequences of Bordetella pertussis,
 RT Bordetella parapertussis and Bordetella bronchiseptica.";
 RL Nat. Genet. 35:32-40(2003).
 -!- FUNCTION: This protein specifically catalyzes the removal of

RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
 RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
 RA Leather S., Moulé S., Norberczak H., O'Neil S., Ormond D., Price C.,
 RA Rabinowitch E., Rutter S., Sanders M., Saunders D., Seeger K.,
 RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
 RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
 RT "Comparative analysis of the genome sequences of Bordetella pertussis,
 RT Bordetella parapertussis and Bordetella bronchiseptica.";
 RL Nat. Genet. 35:32-40(2003).
 -!- FUNCTION: This protein specifically catalyzes the removal of
 CC signal peptides from prolipoproteins (By similarity).
 CC -!- CATALYTIC ACTIVITY: Release of signal peptides from bacterial
 CC membrane prolipoproteins. Hydrolyzes Xaa-Yaa-Zaa-|- (preferably
 CC (S-diacylglyceryl)Cys-, in which xaa is hydrophobic (preferably
 CC Leu), and yaa (Ala or Ser) and zaa (Gly or Ala) have small,
 CC neutral side chains.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -!- SIMILARITY: Belongs to peptidase family A8.
 DR EMBL; BX640416; CAE42039.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004190; F:aspartic-type endopeptidase activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0009005; F:signal peptidase II activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001872; Peptidase_A8.
 DR Pfam; PF01252; Peptidase_A8; 1.
 DR ProDom; PD004304; Peptidase_A8; 1.
 DR TIGRFAMs; TIGR00077; lspA; 1.
 DR PROSITE; PS00855; SPASE II; 1.
 KW Aspartyl protease; Complete proteome; Hydrolase; Lipoprotein;
 KW Protease; Transmembrane.
 SQ SEQUENCE 168 AA; 18829 MW; 1642D83D117C295D CRC64;

Query Match 100.0%; Score 29; DB 2; Length 168;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LPFFD 5
 Db 45 LPFFD 49

RESULT 8
 Q7W8Z3 PRELIMINARY; PRT; 168 AA.
 ID Q7W8Z3
 AC Q7W8Z3
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DE Lipoprotein signal peptidase (EC 3.4.23.36).
 GN Name=lpA; OrderedLocusNames=BPI1983;
 OS Bordetella parapertussis.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Alcaligenaceae; Bordetella.
 OX NCBI_TaxID=519;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=12822 / ATCC BAA-587;
 RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
 RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
 RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
 RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
 RA Achman M., Atkin R., Baker L., Basham D., Bason N., Cherevach I.,
 RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
 RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
 RA Leather S., Moulé S., Norberczak H., O'Neil S., Ormond D., Price C.,
 RA Rabinowitch E., Rutter S., Sanders M., Saunders D., Seeger K.,
 RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
 RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
 RT "Comparative analysis of the genome sequences of Bordetella pertussis,
 RT Bordetella parapertussis and Bordetella bronchiseptica.";
 RL Nat. Genet. 35:32-40(2003).
 -!- FUNCTION: This protein specifically catalyzes the removal of

CC signal peptides from prolipoproteins (By similarity).

CC -1- CATALYTIC ACTIVITY: Release of signal peptides from bacterial

CC membrane prolipoproteins. Hydrolyzes -Xaa-Yaa-Zaa-|-

CC (S,diacylglyceryl)Cys-, in which Xaa is hydrophobic (preferably

CC Leu), and Yaa (Ala or Ser) and Zaa (Gly or Ala) have small,

CC neutral side chains.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

CC EMBL: BX640429; CAE37283.1; -.

DR GO: GO:0004190; F:aspartic-type endopeptidase activity; IEA.

DR GO: GO:0008233; F:peptidase activity; IEA.

DR GO: GO:0009005; F:signal peptidase II activity; IEA.

DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.

DR GO: GO:0009005; F:signal peptidase II activity; IEA.

DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro: IPR001872; Peptidase A8.

DR Pfam: PF01252; Peptidase A8; 1.

DR ProDom: PD004304; Peptidase A8; 1.

DR TIGRFAMs: TIGR00077; lspa; 1.

DR PROSITE: PS00855; SPASE II; 1.

KW Aspartyl protease; Complete proteome; Hydrolase; Lipoprotein;

KW Protease; Transmembrane.

SQ SEQUENCE 168 AA; 18829 MW; FBF41C59833F9875 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 168;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPFFD 5

DB 45 LPFFD 49

RESULT 9

Q7WKD6 PRELIMINARY; PRT; 168 AA.

AC Q7WKD6; 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Lipoprotein signal peptidase (EC 3.4.23.36).

GN Name=lspa; OrderedLocustNames=BB2171;

OS Bordetella bronchiseptica (Alcaligenes bronchiseptica).

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

OC Alcaligenaceae; Bordetella.

OX NCBI_TaxID=518;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=RB50 / ATCC BAA-588;

RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,

RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,

RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Felwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagsels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds S., Skellern J., Squares R., Squares K., Stevens K.,
RA Unwin L., Whitehead S., Barrall B.G., Maskell D.J.,
RT Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.;
RL Nat. Genet. 35:32-40 (2003).

CC -1- FUNCTION: This protein specifically catalyzes the removal of

CC signal peptides from prolipoproteins (By similarity).

CC -1- CATALYTIC ACTIVITY: Release of signal peptides from bacterial

CC membrane prolipoproteins. Hydrolyzes -Xaa-Yaa-Zaa-|-

CC (S,diacylglyceryl)Cys-, in which Xaa is hydrophobic (preferably

CC Leu), and Yaa (Ala or Ser) and Zaa (Gly or Ala) have small,

CC neutral side chains.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

CC EMBL: BX640443; CAE32667.1; -.

DR GO: GO:0004190; F:aspartic-type endopeptidase activity; IEA.

DR GO: GO:0008233; F:peptidase activity; IEA.

DR GO: GO:0009005; F:signal peptidase II activity; IEA.

DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro: IPR001872; Peptidase A8.

DR Pfam: PF01252; Peptidase A8; 1.

DR ProDom: PD004304; Peptidase A8; 1.

DR TIGRFAMs: TIGR00077; lspa; 1.

DR PROSITE: PS00855; SPASE II; 1.

KW Aspartyl protease; Complete proteome; Hydrolase; Lipoprotein;

KW Protease; Transmembrane.

SQ SEQUENCE 168 AA; 18829 MW; FBF41C59833F9875 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 168;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPFFD 5

DB 45 LPFFD 49

RESULT 10

Q6N1M9 PRELIMINARY; PRT; 182 AA.

AC Q6N1M9; 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Signal peptidase II, family A8.

GN Name=lspa; OrderedLocustNames=RPA4376;

OS Rhodopseudomonas palustris.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Bradyrhizobiaceae; Rhodopseudomonas.

OX NCBI_TaxID=1076;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CGA009 / ATCC BAA-98;

RX PubMed=14704707; DOI=10.1038/nbt923;

RA Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,

RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,

RA Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C.,

RA Harrison P.H., Gibson J., Harwood C.S.;

RT "Complete genome sequence of the metabolically versatile

RT photosynthetic bacterium Rhodopseudomonas palustris";

RL Nat. Biotechnol. 22:55-61 (2004).

CC -1- FUNCTION: This protein specifically catalyzes the removal of

CC signal peptides from prolipoproteins (By similarity).

CC -1- CATALYTIC ACTIVITY: Release of signal peptides from bacterial

CC membrane prolipoproteins. Hydrolyzes -Xaa-Yaa-Zaa-|-

CC (S,diacylglyceryl)Cys-, in which Xaa is hydrophobic (preferably

CC Leu), and Yaa (Ala or Ser) and Zaa (Gly or Ala) have small,

CC neutral side chains.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

CC EMBL: BX572607; CAE29817.1; -.

DR GO: GO:0004190; F:aspartic-type endopeptidase activity; IEA.

DR GO: GO:0008233; F:peptidase activity; IEA.

DR GO: GO:0009005; P:proteolysis and peptidolysis; IEA.

DR InterPro: IPR001872; Peptidase A8.

DR Pfam: PF01252; Peptidase A8; 1.

DR PRINTS: PR00781; LIPOSIGPTASE

DR ProDom: PD004304; Peptidase A8; 1.

DR TIGRFAMs: TIGR00077; lspa; 1.

KW Aspartyl protease; Complete proteome; Hydrolase; Protease;

KW Transmembrane.

SQ SEQUENCE 182 AA; 19519 MW; ABACEDD153C3F3F1 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 182;

Best Local Similarity 100.0%; Pred. No. 2.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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Qy 1 LPFFD 5
Db 58 LPFFD 62

RESULT 11
AROK_CHLMU
ID AROK_CHLMU STANDARD; PRT; 184 AA.
AC Q9PR27;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Shikimate kinase (EC 2.7.1.71) (SK).
GN Name=aroK; OrderedLocusNames=rc0646;
OS Chlamydia muridarum.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MoPn / Nig9;
RX MEDLINE=20150255; PubMed=10684935; DOI=10.1093/nar/28.6.1397;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J.D., Utterback T.R., Berry K.J.,
RA Bass S., Linher K.D., Weidman J.F., Khouri H.M., Craven B., Bowman C.,
RA Dodson R.J., Gwin M.L., Nelson W.C., DeBoy R.T., Kolonay J.F.,
RA McClarty G., Salzberg S.L., Eisen J.A., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
CC -!- CATALYTIC ACTIVITY: ATP + shikimate = ADP + shikimate 3-phosphate.
CC -!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC fifth step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: Belongs to the shikimate kinase family.
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CC -----
DR EMBL; AE002332; AAF39473.1; -.
DR PIR; E81679; E81679.
DR HSSP; P10880; 1SHK.
DR TIGR; TC0646; -.
DR HAMAP; MF_00109; -.
DR InterPro; IPR000623; Shik_kinase.
DR Pfam; PF01202; SKI; 1.
DR PRINTS; PR01100; SHIKIMTKINASE.
DR PROSITE; PS01128; SHIKIMATE_KINASE; FALSE NEG.
KW Aromatic amino acid biosynthesis; ATP-binding; Complete proteome;
KW Kinase; Transferase.
FT NP_BIND 14 21 ATP (Potential).
SQ SEQUENCE 184 AA; 20805 MW; 1753812ED7210D9A CRC64;

Query Match 100.0%; Score 29; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPFFD 5
Db 33 LPFFD 37

RESULT 12
AROK_CHLTR
ID AROK_CHLTR STANDARD; PRT; 184 AA.
AC O84372;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

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DE Shikimate kinase (EC 2.7.1.71) (SK).
GN Name=aroK; OrderedLocusNames=CT367;
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D/UM-3/Cx;
RX MEDLINE=99000809; PubMed=9784136; DOI=10.1126/science.282.5389.754;
RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis.";
RL Science 282:754-759(1998).
CC -!- CATALYTIC ACTIVITY: ATP + shikimate = ADP + shikimate 3-phosphate.
CC -!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC fifth step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: Belongs to the shikimate kinase family.
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CC -----
DR EMBL; AE001310; AAC67963.1; -.
DR PIR; H71522; H71522.
DR HSSP; P10880; 1SHK.
DR HAMAP; MF_00109; -.
DR InterPro; IPR000623; Shik_kinase.
DR Pfam; PF01202; SKI; 1.
DR PRINTS; PR01100; SHIKIMTKINASE.
DR PROSITE; PS01128; SHIKIMATE_KINASE; FALSE NEG.
KW Aromatic amino acid biosynthesis; ATP-binding; Complete proteome;
KW Kinase; Transferase.
FT NP_BIND 14 21 ATP (Potential).
SQ SEQUENCE 184 AA; 20512 MW; 8E8CD3EF6AF4A34 CRC64;

Query Match 100.0%; Score 29; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPFFD 5
Db 33 LPFFD 37

RESULT 13
O8XV61
ID O8XV61 PRELIMINARY; PRT; 190 AA.
AC O8XV61;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PROBABLE SHIKIMATE KINASE I PROTEIN (EC 2.7.1.71).
GN Name=aroK; Synonyms=RS01327; OrderedLocusNames=RSc2970;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GMI1000;
RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Sigulier P., Thebault P., Whalen M., Wincker P., Levy M.,

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RA Weissenbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen *Ralstonia solanacearum*."
 RL Nature 415:457-502(2002).
 DR EMBL; AL646073; CAD16679.1; -.
 DR HSSP; P24167; IKAG.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004765; F:shikimate kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0008652; P:amino acid biosynthesis; IEA.
 DR PRINTS; PK01100; SHIKIMINASE.
 DR PROSITE; PS01128; SHIKIMATE KINASE; 1.
 DR PROSITE; PS00267; TACHYKININ; UNKNOWN 1.
 KW Complete proteome; Kinase; Transferase.
 SQ SEQUENCE 190 AA; 21220 MW; 301754E5398B66F6 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 190;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPFFD 5
 Db 29 LPFFD 33

RESULT 14

Q9FD35
 ID Q9FD35 PRELIMINARY; PRT; 192 AA.
 AC Q9FD35;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Pseudomonas putida.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TW3;
 RX MEDLINE=21101804; PubMed=11157934;
 RX DOI=10.1128/JB.183.4.1225-1232.2001;
 RA Hughes M.A., Williams P.A.
 RT "Cloning and characterisation of the pnb genes, encoding enzymes for
 4-nitrobenzoate catabolism in *Pseudomonas putida* TW3."
 RL J. Bacteriol. 183:1225-1232(2001).
 DR EMBL; AF292094; AAG01541.1; -.
 DR InterPro; IPR005025; FMN_red.
 DR Pfam; PF03358; FMN_red; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 192 AA; 20040 MW; C54CBE308842B02D CRC64;

Query Match 100.0%; Score 29; DB 2; Length 192;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPFFD 5
 Db 46 LPFFD 50

RESULT 15

Q890A9
 ID Q890A9 PRELIMINARY; PRT; 200 AA.
 AC Q890A9;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Oxidoreductase (Putative) (EC 1.-.-.-).
 GN OrderedLocusNames=lp_0127;
 OS Lactobacillus plantarum.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxID=1590;

[1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=NCIMB 8826 / WCFS1;
 RX MEDLINE=22480296; PubMed=12566566; DOI=10.1073/pnas.0337704100;
 RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
 RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
 RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
 RA Hofer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
 RA De Vos W.M., Siezen R.J.;
 RT "Complete genome sequence of *Lactobacillus plantarum* WCFS1."
 RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
 DR EMBL; AL935252; CAD62805.1; -.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 KW Complete proteome; Oxidoreductase.
 SQ SEQUENCE 200 AA; 22261 MW; 09D0C16C981B7E1D CRC64;

Query Match 100.0%; Score 29; DB 2; Length 200;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPFFD 5
 Db 49 LPFFD 53

Search completed: November 3, 2005, 08:03:51
 Job time : 175 secs

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OM protein - protein search, using sw model

Run on: November 3, 2005, 07:54:20 ; Search time 41 Seconds
(without alignments)
9.104 Million cell updates/sec

Title: US-10-726-366-1

Perfect score: 29

Sequence: 1 LPFFD 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database :
- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
 - 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
 - 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
 - 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
 - 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	5	2	US-08-630-645-18
2	29	100.0	5	4	US-08-766-596A-18
3	29	100.0	5	4	US-09-241-606-22
4	29	100.0	5	4	US-09-706-540C-1
5	29	100.0	5	4	US-09-861-847A-14
6	29	100.0	5	5	PCT-US96-10220-18
7	29	100.0	217	4	US-09-328-352-7768
8	29	100.0	292	4	US-09-607-745-9
9	29	100.0	406	4	US-09-851-588-6
10	29	100.0	423	4	US-09-656-002-2
11	29	100.0	435	3	US-09-008-271A-6
12	29	100.0	435	4	US-09-607-745-2
13	29	100.0	437	4	US-09-851-588-8
14	29	100.0	440	2	US-08-808-931-24
15	29	100.0	440	3	US-08-808-323-24
16	29	100.0	440	3	US-09-050-603A-24
17	29	100.0	440	3	US-09-102-420B-24
18	29	100.0	440	3	US-09-497-698-24
19	29	100.0	440	4	US-09-730-525-24
20	29	100.0	441	4	US-09-248-796A-18617
21	29	100.0	453	4	US-09-270-767-44855
22	29	100.0	461	4	US-09-538-092-1048
23	29	100.0	481	1	US-08-472-028A-6
24	29	100.0	481	2	US-08-808-931-6
25	29	100.0	481	3	US-08-808-323-6
26	29	100.0	481	3	US-09-050-603A-6
27	29	100.0	481	3	US-09-102-420B-6

28	29	100.0	481	3	US-09-015-683-6	Sequence 6, Appli
29	29	100.0	481	3	US-09-497-698-6	Sequence 6, Appli
30	29	100.0	481	4	US-09-730-525-6	Sequence 6, Appli
31	29	100.0	483	3	US-09-071-296-6	Sequence 6, Appli
32	29	100.0	483	3	US-09-196-268-6	Sequence 6, Appli
33	29	100.0	483	3	US-09-191-998-6	Sequence 6, Appli
34	29	100.0	494	4	US-09-949-016-8778	Sequence 8778, Ap
35	29	100.0	536	2	US-08-808-931-20	Sequence 20, Appl
36	29	100.0	536	3	US-08-808-323-20	Sequence 20, Appl
37	29	100.0	536	3	US-09-050-603A-20	Sequence 20, Appl
38	29	100.0	536	3	US-09-102-420B-20	Sequence 20, Appl
39	29	100.0	536	3	US-09-497-698-20	Sequence 20, Appl
40	29	100.0	536	4	US-09-730-525-20	Sequence 20, Appl
41	29	100.0	537	1	US-08-472-028A-2	Sequence 2, Appli
42	29	100.0	537	2	US-08-808-931-2	Sequence 2, Appli
43	29	100.0	537	3	US-08-808-323-2	Sequence 2, Appli
44	29	100.0	537	3	US-09-050-603A-2	Sequence 2, Appli
45	29	100.0	537	3	US-09-102-420B-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-630-645-18
; Sequence 18, Application US/08630645
; Patent No. 5948763
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,645
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-630-645-18

Query Match 100.0%; Score 29; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 1 LPFFD 5
Db 1 LPFFD 5

RESULT 2
US-08-766-596A-18
; Sequence 18, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-18

Query Match 100.0%; Score 29; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.le+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPFFD 5
Db 1 LPFFD 5

RESULT 3
US-09-241-606-22
; Sequence 22, Application US/09241606
; Patent No. 6472140
; GENERAL INFORMATION:
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Kovacs, Dora

; APPLICANT: Saunders, Aleister J.
; TITLE OF INVENTION: Alpha-2-Macroglobulin Therapies and Drug Screening Methods for
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 0609.4460003
; CURRENT APPLICATION NUMBER: US/09/241,606
; CURRENT FILING DATE: 1999-02-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-241-606-22

Query Match 100.0%; Score 29; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.le+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPFFD 5
Db 1 LPFFD 5

RESULT 4
US-09-706-540C-1
; Sequence 1, Application US/09706540C
; Patent No. 6689753
; GENERAL INFORMATION:
; APPLICANT: Soto-Jara, Claudio
; TITLE OF INVENTION: Peptide Analogs and Mimetics Suitable for in Vivo Use in the Trea
; TITLE OF INVENTION: Diseases Associated with Abnormal Protein Folding etc.
; FILE REFERENCE: 009621-34567
; CURRENT APPLICATION NUMBER: US/09/706,540C
; CURRENT FILING DATE: 2000-11-04
; PRIOR APPLICATION NUMBER: US 60/163,911
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic chemical peptide.
US-09-706-540C-1

Query Match 100.0%; Score 29; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.le+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPFFD 5
Db 1 LPFFD 5

RESULT 5
US-09-861-847A-14
; Sequence 14, Application US/09861847A
; Patent No. 6713450
; GENERAL INFORMATION:
; APPLICANT: FRANGIONE, Blas
; APPLICANT: WISNIEWSKI, Thomas
; APPLICANT: SIGURDSSON, Einar
; TITLE OF INVENTION: SYNTHETIC IMMUNOGENIC BUT NON-AMYLOIDGENIC PEPTIDES
; TITLE OF INVENTION: HOMOLOGOUS TO AMYLOID BETA FOR INDUCTION OF AN IMMUNE
; TITLE OF INVENTION: RESPONSE TO AMYLOID BETA AND AMYLOID DEPOSITS
; FILE REFERENCE: 5986/1K433-US1
; CURRENT APPLICATION NUMBER: US/09/861,847A
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 60/016,233
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0

SEQ ID NO 14
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-861-847A-14

Query Match 100.0%; Score 29; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPFFD 5
DB 1 LPFFD 5

RESULT 6

PCT-US96-10220-18
; Sequence 18, Application PC/TUS9610220
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10220
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US96-10220-18

Query Match 100.0%; Score 29; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPFFD 5
DB 1 LPFFD 5

RESULT 7

US-09-328-352-7768
; Sequence 7768, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7768
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7768

Query Match 100.0%; Score 29; DB 4; Length 217;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPFFD 5
DB 58 LPFFD 62

RESULT 8

US-09-607-745-9
; Sequence 9, Application US/09607745
; Patent No. 6750034
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew L
; APPLICANT: Qi, Jain-shen
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: DNA encoding human serine protease D-G
; FILE REFERENCE: ORT-1273
; CURRENT APPLICATION NUMBER: US/09/607,745
; CURRENT FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 9
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
US-09-607-745-9

Query Match 100.0%; Score 29; DB 4; Length 292;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPFFD 5
DB 158 LPFFD 162

RESULT 9

US-09-851-588-6
; Sequence 6, Application US/09851588
; Patent No. 6682890
; GENERAL INFORMATION:
; APPLICANT: Mack, David
; APPLICANT: Gish, Kurt C.
; APPLICANT: Wilson, Keith E.
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AND
; TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER MODULATORS
; FILE REFERENCE: A-68829-1/DJB/JJD/AMS
; CURRENT APPLICATION NUMBER: US/09/851,588
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 09/642,252
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: US 09/656,002

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; PRIOR FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-851-588-6

Query Match      100.0%; Score 29; DB 4; Length 406;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 LPFFD 5
Db      280 LPFFD 284

RESULT 10
US-09-656-002-2
; Sequence 2, Application US/09656002
; Patent No. 6455668
; GENERAL INFORMATION:
; APPLICANT: Mack, David
; APPLICANT: Gish, Kurt
; APPLICANT: Wilson, Keith
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AND
; TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER MODULATORS
; FILE REFERENCE: A-69108/DJB/JJD/AMS
; CURRENT APPLICATION NUMBER: US/09/656,002
; CURRENT FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 09/525,993
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: US 09/493,444
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: PCT/US 00/07044
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-656-002-2

Query Match      100.0%; Score 29; DB 4; Length 423;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 LPFFD 5
Db      297 LPFFD 301

RESULT 11
US-09-008-271A-6
; Sequence 6, Application US/09008271A
; Patent No. 6203979
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Tang, Tom Y.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA

; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,271A
; FILING DATE: 16-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mohan-Peterson, Sheela
; REGISTRATION NUMBER: 41,201
; REFERENCE/DOCKET NUMBER: PF-0458 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 435 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: COLNNOT13
; CLONE: 1337018
; SEQUENCE DESCRIPTION: SEQ ID NO: 6 :
US-09-008-271A-6

Query Match      100.0%; Score 29; DB 3; Length 435;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 LPFFD 5
Db      309 LPFFD 313

RESULT 12
US-09-607-745-2
; Sequence 2, Application US/09607745
; Patent No. 6750034
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew L
; APPLICANT: Qi, Jain-shen
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: DNA encoding human serine protease D-G
; FILE REFERENCE: ORT-1273
; CURRENT APPLICATION NUMBER: US/09/607,745
; CURRENT FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-607-745-2

Query Match      100.0%; Score 29; DB 4; Length 435;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 LPFFD 5
Db      309 LPFFD 313

RESULT 13
US-09-851-588-8
; Sequence 8, Application US/09851588
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; Patent No. 6682890
; GENERAL INFORMATION:
; APPLICANT: Mack, David
; APPLICANT: Gish, Kurt C.
; APPLICANT: Wilson, Keith E.
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AND
; TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER MODULATORS
; FILE REFERENCE: A-68829-1/DJB/JJD/AWS
; CURRENT APPLICATION NUMBER: US/09/851.588
; CURRENT FILING DATE: 2001-09-24
; PRIOR FILING DATE: 2000-08-17
; PRIOR FILING DATE: 2000-09-06
; PRIOR FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-851-588-8

Query Match 100.0%; Score 29; DB 4; Length 437;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPFFD 5
Db 311 LPFFD 315

RESULT 14

US-08-808-931-24
; Sequence 24, Application US/08808931
; Patent No. 5939602
; GENERAL INFORMATION:
; APPLICANT: Volrath, Sandra
; APPLICANT: Johnson, Marie
; APPLICANT: Potter, Sharon
; APPLICANT: Ward, Eric
; APPLICANT: Heifetz, Peter
; TITLE OF INVENTION: DNA Molecules Encoding Plant
; TITLE OF INVENTION: Protoporphyrinogen Oxidase and Inhibitor-Resistant Mutants
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5939602artis Corporation
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,931
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/012,705
; FILING DATE: 28-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,612
; FILING DATE: 28-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/020,003
; FILING DATE: 21-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 36,241

; REFERENCE/DOCKET NUMBER: CGC 1847
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 440 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
US-08-808-931-24

Query Match 100.0%; Score 29; DB 2; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPFFD 5
Db 65 LPFFD 69

RESULT 15

US-08-808-323-24
; Sequence 24, Application US/08808323
; Patent No. 6018105
; GENERAL INFORMATION:
; APPLICANT: Johnson, Marie
; APPLICANT: Volrath, Sandra
; APPLICANT: Ward, Eric
; TITLE OF INVENTION: Promoters from Plant
; TITLE OF INVENTION: Protoporphyrinogen Oxidase Genes
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6018105artis Corporation
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,323
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/012,705
; FILING DATE: 28-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,612
; FILING DATE: 28-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/020,003
; FILING DATE: 21-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 36,241
; REFERENCE/DOCKET NUMBER: CGC 1846
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 440 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
US-08-808-323-24

Query Match 100.0%; Score 29; DB 3; Length 440;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPFD 5
 Db 65 LPPFD 69

Search completed: November 3, 2005, 08:05:21
 Job time : 44 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 3, 2005, 07:58:16 ; Search time 170 Seconds
(without alignments)
12.306 Million cell updates/sec

Title: US-10-726-366-1

Perfect score: 29

Sequence: 1 LPFFD 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	29	100.0	5	9	US-09-861-847-14
2	29	100.0	5	13	US-10-052-817-22
3	29	100.0	5	14	US-10-235-483-18
4	29	100.0	5	14	US-10-301-488A-14
5	29	100.0	5	15	US-10-666-423-14
6	29	100.0	5	15	US-10-235-852-18
7	29	100.0	5	15	US-10-301-448-14
8	29	100.0	5	16	US-10-726-366-1
9	29	100.0	5	17	US-10-464-117-15
10	29	100.0	5	17	US-10-933-206-52
11	29	100.0	5	18	US-10-497-160-43

12	29	100.0	5	20	US-11-004-053-52	Sequence 52, Appl
13	29	100.0	5	20	US-11-007-643-52	Sequence 52, Appl
14	29	100.0	5	20	US-11-007-644-52	Sequence 52, Appl
15	29	100.0	5	20	US-11-007-669-52	Sequence 52, Appl
16	29	100.0	6	17	US-10-464-117-167	Sequence 167, App
17	29	100.0	63	16	US-10-425-115-252821	Sequence 252821,
18	29	100.0	72	16	US-10-425-115-295526	Sequence 295526,
19	29	100.0	77	16	US-10-425-115-280256	Sequence 280256,
20	29	100.0	82	15	US-10-424-599-269312	Sequence 269312,
21	29	100.0	92	15	US-10-424-599-148411	Sequence 148411,
22	29	100.0	118	16	US-10-425-115-318552	Sequence 318552,
23	29	100.0	128	15	US-10-424-599-21854	Sequence 21854,
24	29	100.0	132	15	US-10-424-599-213287	Sequence 213287,
25	29	100.0	142	16	US-10-425-115-208603	Sequence 208603,
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27	29	100.0	144	16	US-10-425-115-208600	Sequence 208600,
28	29	100.0	144	20	US-11-111-953-186	Sequence 186, App
29	29	100.0	147	15	US-10-424-599-238931	Sequence 238931,
30	29	100.0	169	14	US-10-106-698-6322	Sequence 6322, Ap
31	29	100.0	189	16	US-10-425-115-208607	Sequence 208607,
32	29	100.0	202	9	US-09-738-636-5797	Sequence 5797, Ap
33	29	100.0	203	15	US-10-424-599-225293	Sequence 225293,
34	29	100.0	227	16	US-10-437-963-170604	Sequence 170604,
35	29	100.0	228	16	US-10-437-963-106374	Sequence 106374,
36	29	100.0	231	16	US-10-425-115-232722	Sequence 232722,
37	29	100.0	267	16	US-10-425-115-316816	Sequence 316816,
38	29	100.0	265	15	US-10-425-114-68749	Sequence 68749, A
39	29	100.0	265	16	US-10-425-115-316814	Sequence 316814,
40	29	100.0	273	15	US-10-425-114-68748	Sequence 68748, A
41	29	100.0	290	15	US-10-425-114-69996	Sequence 69996, A
42	29	100.0	292	18	US-10-803-530-9	Sequence 9, Appli
43	29	100.0	306	20	US-11-097-143-24576	Sequence 24576, A
44	29	100.0	307	15	US-10-425-114-51112	Sequence 51112, A
45	29	100.0	313	16	US-10-788-792-235	Sequence 235, App

ALIGNMENTS

RESULT 1
US-09-861-847-14
; Sequence 14, Application US/09861847
; Patent No. US2002007288A1
; GENERAL INFORMATION:
; APPLICANT: FRANGIONE, Blas
; APPLICANT: WISNIEWSKI, Thomas
; APPLICANT: SIGURDSSON, Einar
; TITLE OF INVENTION: SYNTHETIC IMMUNOGENIC BUT NON-AMYLOIDGENIC PEPTIDES FOR INDUCTION OF AN IMMUNE RESPONSE TO AMYLOID BETA
; TITLE OF INVENTION: AMYLOID BETA FOR INDUCTION OF AN IMMUNE RESPONSE TO AMYLOID DEPOSITS
; FILE REFERENCE: FRANGIONE=2A
; CURRENT APPLICATION NUMBER: US/09/861,847
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 60/016,233
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-861-847-14

Query Match 100.0%; Score 29; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPFFD 5

Db i LPFFD 5

```

; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-235-483-18

Query Match 100.0%; Score 29; DB 14; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPFFD 5
Db 1 LPFFD 5

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US-10-301-488A-14
; Sequence 14, Application US/10301488A
; Publication No. US20030166558A1
; GENERAL INFORMATION:
; APPLICANT: FRANGIONE, Blas
; APPLICANT: WISNIEWSKI, Thomas
; APPLICANT: SIGURDSSON, Einar
; TITLE OF INVENTION: SYNTHETIC IMMUNOGENIC BUT NON-DEPOSIT-FORMING POLYPEPTIDES AND
; TITLE OF INVENTION: PEPTIDES HOMOLOGOUS TO AMYLOID BETA, PRION PROTEIN, AMYLIN, AN
; TITLE OF INVENTION: ALPHA-SYNUCLEIN, OR POLYGLUTAMINE REPEATS FOR INDUCTION OF AN
; TITLE OF INVENTION: IMMUNE RESPONSE THEROY
; FILE REFERENCE: 5986/1K434US1
; CURRENT APPLICATION NUMBER: US/10/301,488A
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/331,801
; PRIOR FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-301-488A-14

Query Match 100.0%; Score 29; DB 14; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPFFD 5
Db 1 LPFFD 5

RESULT 5
US-10-666-423-14
; Sequence 14, Application US/10666423
; Publication No. US20040043935A1
; GENERAL INFORMATION:
; APPLICANT: FRANGIONE, Blas
; APPLICANT: WISNIEWSKI, Thomas
; APPLICANT: SIGURDSSON, Einar
; TITLE OF INVENTION: SYNTHETIC IMMUNOGENIC BUT NON-AMYLOIDOGNIC PEPTIDES
; TITLE OF INVENTION: HOMOLOGOUS TO AMYLOID BETA FOR INDUCTION OF AN IMMUNE
; TITLE OF INVENTION: RESPONSE TO AMYLOID BETA AND AMYLOID DEPOSITS

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FILE REFERENCE: 5986/1K433-US1
 CURRENT APPLICATION NUMBER: US/10/666,423
 PRIOR FILING DATE: 2003-09-19
 PRIOR APPLICATION NUMBER: US/09/861,847A
 PRIOR FILING DATE: 2001-05-22
 PRIOR APPLICATION NUMBER: 60/016,233
 PRIOR FILING DATE: 2000-05-22
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 14
 LENGTH: 5
 TYPE: PRT
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: Synthetic
 US-10-666-423-14

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 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPFFD 5
 DB 1 LPFFD 5

RESULT 6

US-10-235-852-18
 Sequence 18, Application US/10235852
 Publication No. US20040052928A1
 GENERAL INFORMATION:
 APPLICANT: Gazit, Ehud
 TITLE OF INVENTION: PEPTIDES AND METHODS USING SAME FOR DIAGNOSING AND TREATING AMYLOID
 FILE OF INVENTION: ASSOCIATED DISEASES
 FILE REFERENCE: 02/23654
 CURRENT APPLICATION NUMBER: US/10/235,852
 CURRENT FILING DATE: 2002-09-06
 NUMBER OF SEQ ID NOS: 23
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 18
 LENGTH: 5
 TYPE: PRT
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: Beta-amyloid peptide derived, active site sequence
 US-10-235-852-18

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 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPFFD 5
 DB 1 LPFFD 5

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US-10-301-448-14
 Sequence 14, Application US/10301448
 Publication No. US20040095964A1
 GENERAL INFORMATION:
 APPLICANT: FRANGIONE, Blas
 APPLICANT: WISNIEWSKI, Thomas
 APPLICANT: SIGURDSSON, Einar
 TITLE OF INVENTION: SYNTHETIC IMMUNOGENIC BUT NON-DEPOSIT-FORMING POLYPEPTIDES AND
 TITLE OF INVENTION: PEPTIDES HOMOLOGOUS TO AMYLOID BETA, PRION PROTEIN, AMYLIN,
 TITLE OF INVENTION: ALPHA-SYNUCLEIN, OR POLYGLUTAMINE REPEATS FOR INDUCTION OF AN
 TITLE OF INVENTION: IMMUNE RESPONSE THERETO
 FILE REFERENCE: 5986/1K434US1
 CURRENT APPLICATION NUMBER: US/10/301,448
 CURRENT FILING DATE: 2003-02-21
 PRIOR APPLICATION NUMBER: US 60/331,801
 PRIOR FILING DATE: 2001-11-21

NUMBER OF SEQ ID NOS: 55
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 14
 LENGTH: 5
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic
 US-10-301-448-14

Query Match 100.0%; Score 29; DB 15; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
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QY 1 LPFFD 5
 DB 1 LPFFD 5

RESULT 8

US-10-726-366-1
 Sequence 1, Application US/10726366
 Publication No. US20040121960A1
 GENERAL INFORMATION:
 APPLICANT: Soto-Jara, Claudio
 TITLE OF INVENTION: Peptide Analogs and Mimetics Suitable for in Vivo Use in the Trea
 FILE OF INVENTION: Diseases Associated with Abnormal Protein Folding etc.
 FILE REFERENCE: 009621-34567
 CURRENT APPLICATION NUMBER: US/10/726,366
 CURRENT FILING DATE: 2003-12-03
 PRIOR APPLICATION NUMBER: US 60/163,911
 PRIOR FILING DATE: 1999-11-05
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 1
 LENGTH: 5
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic chemical peptide.
 US-10-726-366-1

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QY 1 LPFFD 5
 DB 1 LPFFD 5

RESULT 9

US-10-464-117-15
 Sequence 15, Application US/10464117
 Publication No. US20050014193A1
 GENERAL INFORMATION:
 APPLICANT: Palatin Technologies, Inc.
 APPLICANT: Sharma, Shubb D.
 APPLICANT: Shi, Yi-Qun
 TITLE OF INVENTION: Identification of Target-Specific Folding Sites in Peptides and
 TITLE OF INVENTION: Proteins
 FILE REFERENCE: 70025-UT-50075
 CURRENT APPLICATION NUMBER: US/10/464,117
 CURRENT FILING DATE: 2003-06-17
 PRIOR APPLICATION NUMBER: PCT/US01/50075
 PRIOR FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: US 60/256,842
 PRIOR FILING DATE: 2000-12-19
 PRIOR APPLICATION NUMBER: US 60/304,835
 PRIOR FILING DATE: 2001-02-13
 PRIOR APPLICATION NUMBER: US 60/327,835
 PRIOR FILING DATE: 2001-10-04
 NUMBER OF SEQ ID NOS: 171

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; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; PRIOR APPLICATION NUMBER: 60/027,981
; PRIOR FILING DATE: 1996-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 52
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-007-643-52

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Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 LPFFD 5

RESULT 14
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; Sequence 52, Application US/11007644
; Publication No. US20050153897A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; FILE REFERENCE: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
; CURRENT APPLICATION NUMBER: US/11/007,644
; CURRENT FILING DATE: 2004-12-07
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; PRIOR APPLICATION NUMBER: 60/027,981
; PRIOR FILING DATE: 1996-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 52
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-007-644-52

Query Match 100.0%; Score 29; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 LPFFD 5

RESULT 15
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; Sequence 52, Application US/11007669
; Publication No. US20050153898A1
; GENERAL INFORMATION:

; APPLICANT: CASTILLO, GERARDO
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; FILE REFERENCE: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
; CURRENT APPLICATION NUMBER: US/11/007,669
; CURRENT FILING DATE: 2004-12-07
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; PRIOR APPLICATION NUMBER: 60/027,981
; PRIOR FILING DATE: 1996-10-08
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; LENGTH: 5
; TYPE: PRT
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 LPFFD 5

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